

#7

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U.S. PATENT AND TRADEMARK OFFICE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/848,035

DATE: 09/21/2001  
TIME: 18:04:35

Input Set : A:\SEQUENCE LISTING.TXT  
Output Set: N:\CRF3\09212001\I848035.raw

4 <110> APPLICANT: Bertin, John  
 6 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE NBS/LRR PROTEIN FAMILY AND USES  
 THEREOF  
 8 <130> FILE REFERENCE: 07334-268001  
 10 <140> CURRENT APPLICATION NUMBER: US 09/848,035  
 11 <141> CURRENT FILING DATE: 2001-05-03  
 13 <150> PRIOR APPLICATION NUMBER: US 60/201,464  
 14 <151> PRIOR FILING DATE: 2000-05-03  
 16 <160> NUMBER OF SEQ ID NOS: 17  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 2464  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (1)...(2463)  
 29 <400> SEQUENCE: 1  
 30 atg aca tcg ccc cag cta gag tgg act ctg cag acc ctt ctg gag cag 48  
 31 Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln  
 32 1 5 10 15  
 34 ctg aac gag gat gaa tta aag agt ttc aaa tcc ctt tta tgg gct ttt 96  
 35 Leu Asn Glu Asp Glu Leu Lys Ser Phe Lys Ser Leu Leu Trp Ala Phe  
 36 20 25 30  
 38 ccc ctc gaa gac gtg cta cag aag acc cca tgg tct gag gtg gaa gag 144  
 39 Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu  
 40 35 40 45  
 42 gct gat ggc aag aaa ctg gca gaa att ctg gtc aac acc tcc tca gaa 192  
 43 Ala Asp Gly Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu  
 44 50 55 60  
 46 aat tgg ata agg aat gcg act gtg aac atc ttg gaa gag atg aat ctc 240  
 47 Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu  
 48 65 70 75 80  
 50 acg gaa ttg tgt aag atg gca aag gct gag atg atg gag gac gga cag 288  
 51 Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln  
 52 85 90 95  
 54 gtg caa gaa ata gat aat cct gag ctg gga gat gca gaa gaa gac tcg 336  
 55 Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser  
 56 100 105 110  
 58 gag tta gca aag cca ggt gaa aag gga tgg aga aat tca atg gag 384  
 59 Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu  
 60 115 120 125  
 62 aaa caa tct ttg gtc tgg aag aac acc ttt tgg caa gga gac att gac 432  
 63 Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp  
 64 130 135 140  
 66 aat ttc cat gac gac gtc act ctg aga aac caa cgg ttc att cca ttc 480  
 67 Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe  
 68 145 150 155 160

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70	ttg aat ccc aga aca ccc agg aag cta aca cct tac acg gtg gtg ctg	528
71	Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu	
72	165 170 175	
74	cac ggc ccc gca ggc gtg ggg aaa acc acg ctg gcc aaa aag tgt atg	576
75	His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met	
76	180 185 190	
78	ctg gac tgg aca gac tgc aac ctc acg ccg acg ctc aga tac gcg ttc	624
79	Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe	
80	195 200 205	
82	tac ctc agc tgc aag gag ctc agc cgc atg ggc ccc tgc agt ttt gca	672
83	Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala	
84	210 215 220	
86	gag ctg atc tcc aaa gac tgg cct gaa ttg cag gat gac att cca agc	720
87	Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser	
88	225 230 235 240	
90	atc cta gcc caa gca cag aga atc ctg ttc gtg gtc gat ggc ctt gat	768
91	Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp	
92	245 250 255	
94	gag ctg aaa gtc cca cct ggg gcg ctg atc cag gac atc tgc ggg gac	816
95	Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp	
96	260 265 270	
98	tgg gag aag aag ccg gtg ccc gtc ctc ctg ggg agt ttg ctg aag	864
99	Trp Glu Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys	
100	275 280 285	
102	agg aag atg tta ccc agg gca gcc ttg ctg gtc acc acg cgg ccc agg	912
103	Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg	
104	290 295 300	
106	gca ctg agg gac ctc cag ctc ctg gcg cag cag ccg atc tac ata agg	960
107	Ala Leu Arg Asp Leu Gln Leu Ala Gln Gln Pro Ile Tyr Ile Arg	
108	305 310 315 320	
110	gtg gag ggc ttc ctg gag gag gac agg agg gcc tat ttc ctg aga cac	1008
111	Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His	
112	325 330 335	
114	ttt gga gac gag gac caa gcc atg cgt gcc ttt gag cta atg agg agc	1056
115	Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser	
116	340 345 350	
118	aac gcg gcc ctg ttc cag ctg ggc tcg gcc ccc gcg gtg tgc tgg att	1104
119	Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile	
120	355 360 365	
122	gtg tgc acg act ctg aag ctg cag atg gag aag ggg gag gac ccg ccg	1152
123	Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro	
124	370 375 380	
126	gtt ccc gca ggg cgcc aca gct gcg ggg cgcc gct gcg gac gct gag cct	1200
127	Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro	
128	385 390 395 400	
130	cct ggc cgcc gca ggg ctg tgg gcg cag atg tcc gtg ttc cac cga gag	1248
131	Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu	
132	405 410 415	
134	gac ctg gaa agg ctc ggg gtg cag gag tcc gac ctc cgt ctg ttc ctg	1296

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135	Asp	Leu	Glu	Arg	Leu	Gly	Val	Gln	Glu	Ser	Asp	Leu	Arg	Leu	Phe	Leu	
136		420				425									430		
138	gac	gga	gac	atc	ctc	cgc	cag	cag	aga	gtc	tcc	aaa	ggc	tgc	tac	tcc	1344
139	Asp	Gly	Asp	Ile	Leu	Arg	Gln	Asp	Arg	Val	Ser	Lys	Gly	Cys	Tyr	Ser	
140		435				440									445		
142	ttc	atc	cac	ctc	agc	ttc	cag	cag	ttt	ctc	act	gcc	ctg	ttc	tac	gcc	1392
143	Phe	Ile	His	Leu	Ser	Phe	Gln	Gln	Phe	Leu	Thr	Ala	Leu	Phe	Tyr	Ala	
144		450				455									460		
146	ctg	gag	aag	gag	gag	gag	gac	agg	gac	ggc	cac	gcc	tgg	gac	att		1440
147	Leu	Glu	Lys	Glu	Glu	Glu	Glu	Asp	Arg	Asp	Gly	His	Ala	Trp	Asp	Ile	
148	465		470				475								480		
150	ggg	gac	gta	cag	aag	ctg	ctt	tcc	gga	gaa	aga	ctc	aag	aac	ccc		1488
151	Gly	Asp	Val	Gln	Lys	Leu	Leu	Ser	Gly	Glu	Glu	Arg	Leu	Lys	Asn	Pro	
152		485				490									495		
154	gac	ctg	att	caa	gta	gga	cac	ttc	tta	ttc	ggc	ctc	gct	aac	gag	aag	1536
155	Asp	Leu	Ile	Gln	Val	Gly	His	Phe	Leu	Phe	Gly	Leu	Ala	Asn	Glu	Lys	
156		500				505									510		
158	aga	gcc	aag	gag	ttg	gag	gcc	act	ttt	ggc	tgc	cg	atg	tca	ccg	gac	1584
159	Arg	Ala	Lys	Glu	Leu	Glu	Ala	Thr	Phe	Gly	Cys	Arg	Met	Ser	Pro	Asp	
160		515				520									525		
162	atc	aaa	cag	gaa	ttg	ctg	caa	tgc	aaa	gca	cat	ctt	cat	gca	aat	aag	1632
163	Ile	Lys	Gln	Glu	Leu	Leu	Gln	Cys	Lys	Ala	His	Leu	His	Ala	Asn	Lys	
164		530				535									540		
166	ccc	tta	tcc	gtg	acc	gac	ctg	aag	gag	gtc	ttg	ggc	tgc	ctg	tat	gag	1680
167	Pro	Leu	Ser	Val	Thr	Asp	Leu	Lys	Glu	Val	Leu	Gly	Cys	Leu	Tyr	Glu	
168	545		550				555								560		
170	tct	cag	gag	gag	ctg	gcf	aag	gtg	gtg	gtg	gcc	ccg	ttc	aag	gaa		1728
171	Ser	Gln	Glu	Glu	Leu	Ala	Lys	Val	Val	Val	Ala	Pro	Phe	Lys	Glu		
172		565				570									575		
174	att	tct	att	cac	ctg	aca	aat	act	tct	gaa	gtg	atg	cat	tgt	tcc	ttc	1776
175	Ile	Ser	Ile	His	Leu	Thr	Asn	Thr	Ser	Glu	Val	Met	His	Cys	Ser	Phe	
176		580				585									590		
178	agc	ctg	aag	cat	tgt	caa	gac	ttg	cag	aaa	ctc	tca	ctg	cag	gta	gca	1824
179	Ser	Leu	Lys	His	Cys	Gln	Asp	Leu	Gln	Lys	Leu	Ser	Leu	Gln	Val	Ala	
180		595				600									605		
182	aag	ggg	gtg	ttc	ctg	gag	aat	tac	atg	gat	ttt	gaa	ctg	gac	att	gaa	1872
183	Lys	Gly	Val	Phe	Leu	Glu	Asn	Tyr	Met	Asp	Phe	Glu	Leu	Asp	Ile	Glu	
184		610				615									620		
186	ttt	gaa	agc	tca	aac	agc	aac	ctc	aag	ttt	ctg	gaa	gtg	aaa	caa	agc	1920
187	Phe	Glu	Ser	Ser	Asn	Asn	Ser	Leu	Lys	Phe	Leu	Glu	Val	Lys	Gln	Ser	
188	625		630				635								640		
190	ttc	ctg	agt	gac	tct	tct	gtg	cg	att	ctt	tgt	gac	cac	gta	acc	cgt	1968
191	Phe	Leu	Ser	Asp	Ser	Ser	Val	Arg	Ile	Leu	Cys	Asp	His	Val	Thr	Arg	
192		645				650									655		
194	agc	acc	tgt	cat	ctg	cag	aaa	gtg	gag	att	aaa	aac	gtc	acc	cct	gac	2016
195	Ser	Thr	Cys	His	Leu	Gln	Lys	Val	Glu	Ile	Lys	Asn	Val	Thr	Pro	Asp	
196		660				665									670		
198	acc	gcg	tac	cg	gac	ttc	tgt	ctt	gtc	att	ggg	aag	aag	acc	ctc		2064
199	Thr	Ala	Tyr	Arg	Asp	Phe	Cys	Leu	Ala	Phe	Ile	Gly	Lys	Lys	Thr	Leu	

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200	675	680	685	
202	acg cac ctg acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg			2112
203	Thr His Leu Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met			
204	690	695	700	
206	ctg atg ctg tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac			2160
207	Leu Met Leu Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr			
208	705	710	715	720
210	ctg agg ttg gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc			2208
211	Leu Arg Leu Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe			
212	725	730	735	
214	tcc tat gtc ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca			2256
215	Phe Tyr Val Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser			
216	740	745	750	
218	gcc aat gtg ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg			2304
219	Ala Asn Val Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met			
220	755	760	765	
222	aca cgc cca aaa cac ttc ctg cag atg ttg tcg ttg gaa aac tgt cgt			2352
223	Thr Arg Pro Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg			
224	770	775	780	
226	ctt aca gaa gcc agt tgc aag gac ctt gct gct gtc ttg gtt gtc agc			2400
227	Leu Thr Glu Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser			
228	785	790	795	800
230	aag aag ctg aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca			2448
231	Lys Lys Leu Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr			
232	805	810	815	
234	ggg gtg aag ttt ctg t			2464
235	Gly Val Lys Phe Leu			
236	820			
238	<210> SEQ ID NO: 2			
239	<211> LENGTH: 821			
240	<212> TYPE: PRT			
241	<213> ORGANISM: Homo sapiens			
243	<400> SEQUENCE: 2			
244	Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln			
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246	Leu Asn Glu Asp Glu Leu Lys Ser Phe Lys Ser Leu Leu Trp Ala Phe			
247	20	25	30	
248	Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu			
249	35	40	45	
250	Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu			
251	50	55	60	
252	Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu			
253	65	70	75	80
254	Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln			
255	85	90	95	
256	Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser			
257	100	105	110	
258	Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu			
259	115	120	125	

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260 Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp  
 261 130 135 140  
 262 Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe  
 263 145 150 155 160  
 264 Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu  
 265 165 170 175  
 266 His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met  
 267 180 185 190  
 268 Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe  
 269 195 200 205  
 270 Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala  
 271 210 215 220  
 272 Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser  
 273 225 230 235 240  
 274 Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp  
 275 245 250 255  
 276 Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp  
 277 260 265 270  
 278 Trp Glu Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys  
 279 275 280 285  
 280 Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg  
 281 290 295 300  
 282 Ala Leu Arg Asp Leu Gln Leu Ala Gln Gln Pro Ile Tyr Ile Arg  
 283 305 310 315 320  
 284 Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His  
 285 325 330 335  
 286 Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser  
 287 340 345 350  
 288 Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile  
 289 355 360 365  
 290 Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro  
 291 370 375 380  
 292 Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro  
 293 385 390 395 400  
 294 Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu  
 295 405 410 415  
 296 Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu  
 297 420 425 430  
 298 Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser  
 299 435 440 445  
 300 Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Ala  
 301 450 455 460  
 302 Leu Glu Lys Glu Glu Glu Asp Arg Asp Gly His Ala Trp Asp Ile  
 303 465 470 475 480  
 304 Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn Pro  
 305 485 490 495  
 306 Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu Lys  
 307 500 505 510  
 308 Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp

**VERIFICATION SUMMARY**

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